

We claim:

1. A method of isolating a region of genomic DNA associated with a phenotype of interest comprising:

5 (A) identifying an *Arabidopsis* plant of a first ecotype with a phenotype of interest;

(B) crossing said *Arabidopsis* plant with an *Arabidopsis* plant of a second ecotype lacking said phenotype;

(C) propagating and self pollinating seeds from said cross;

(D) selecting progeny of self pollinated seeds with said phenotype;

10 (E) screening progeny of self pollinated seeds with said phenotype with a collection of nucleic acid molecules, said collection of nucleic acid molecules capable of detecting a set of polymorphisms where the polymorphisms are distributed throughout the genome of said self pollinated seeds with said phenotype at an average density of more than one polymorphism per about 100kb, wherein at least one of the polymorphisms is  
15 selected from Table A;

(F) calculating the linkage of each of said polymorphisms to said phenotype;

and

(G) isolating said region of genomic DNA associated with said phenotype based on its linkage to one or more of said nucleic acid molecules.

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2. The method of isolating a region of genomic DNA associated with a phenotype of interest according to claim 1, wherein said region of genomic DNA associated with said phenotype is located between about 5 and about 10 cM of one or more of said polymorphisms.

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3. The method of isolating a region of genomic DNA associated with a phenotype of interest according to claim 1, wherein said region of genomic DNA associated with said

phenotype is located between about 0 and about 5 cM of one or more of said polymorphisms.

4. A method of identifying a region of genomic DNA associated with a phenotypic trait of interest comprising:

(A) screening a mapping population of *Arabidopsis* plants to determine the linkage of said phenotypic trait with a collection of nucleic acid molecules, wherein said nucleic acid molecules are capable of detecting a set of polymorphisms, where the polymorphisms are distributed throughout the genome of said mapping population of *Arabidopsis* plants at an average density of more than one polymorphism per about 100kb, wherein at least one of the polymorphisms is selected from Table A;

(B) calculating the linkage of each of said polymorphisms to said phenotypic trait; and

(C) identifying said genomic DNA region associated said phenotypic trait based on its linkage to one or more of said nucleic acid molecules.

5. The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 4, further comprising isolating said identified region.

6. The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 4, wherein said collection of nucleic acid molecules is capable of detecting a set of greater than 25 polymorphisms selected from Table A.

7. The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 6, wherein said collection of nucleic acid molecules is capable of detecting a set of greater than 50 polymorphisms selected from Table A.

8. The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 7, wherein said collection of nucleic acid molecules is capable of detecting a set of greater than 75 polymorphism selected from Table A.

5 9. The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 8, wherein said collection of nucleic acid molecules is capable of detecting a set of greater than 100 polymorphisms selected from Table A.

10 10. A method of identifying a nucleic acid molecule associated with a phenotypic trait of interest comprising:

(A) screening a mapping population of *Arabidopsis* plants to determine the linkage of said phenotypic trait with a collection of polymorphisms, wherein said polymorphisms are distributed throughout the genome of said mapping population of *Arabidopsis* plants at an average density of more than one polymorphism per about  
15 100kb, wherein at least one of the polymorphisms is selected from Table A;

(B) calculating the linkage of each of said polymorphism to said phenotypic trait; and

(C) isolating said nucleic acid molecule associated with said phenotypic trait based on its linkage to one or more of said polymorphisms.

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11. The method of identifying a nucleic acid molecule associated with a phenotypic trait of interest according to claim 10, wherein said collection of polymorphisms comprises at least 25 polymorphisms selected from Table A.

25 12. The method of identifying a nucleic acid molecule associated with a phenotypic trait of interest according to claim 11, wherein said collection of polymorphisms comprises at least 50 polymorphisms selected from Table A.

13. The method of identifying a nucleic acid molecule associated with a phenotypic trait of interest according to claim 12, wherein said collection of polymorphisms comprises at least 75 polymorphisms selected from Table A.

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14. The method of identifying a nucleic acid molecule associated with a phenotypic trait of interest according to claim 13, wherein said collection of polymorphisms comprises at least 100 polymorphisms selected from Table A.

10 15. The method of identifying a nucleic acid molecule associated with a phenotypic trait of interest according to claim 10, wherein said nucleic acid molecule associated with said phenotypic trait is located between about 5 and about 10 cM of one or more of said polymorphisms.

15 16. The method of identifying a nucleic acid molecule associated with a phenotypic trait of interest according to claim 15, wherein said nucleic acid molecule associated with said phenotypic trait is located between about 0 and about 5 cM of one or more of said polymorphisms.

20 17. A method of isolating a nucleic acid molecule associated with a phenotypic trait comprising:

(A) screening a mapping population of *Arabidopsis* plants to determine the linkage of said phenotypic trait with a collection of polymorphisms, wherein said at least one polymorphism is selected from Table A; and

25 (B) isolating said nucleic acid molecule associated with said phenotypic trait based on its linkage to one or more of said polymorphisms.

18. A collection of non-identical nucleic acid molecules capable of detecting polymorphisms present in an *Arabidopsis* mapping population, wherein said collection of non-identical nucleic acid molecules is capable of detecting at least 25 polymorphisms  
5 selected from the group consisting of Table A.

19. The collection of non-identical nucleic acid molecules capable of detecting polymorphisms present in an *Arabidopsis* mapping population according to claim 18, wherein said collection non-identical nucleic acid molecules is capable of detecting at  
10 least 25 polymorphisms which are single nucleotide polymorphisms.

20. The collection of non-identical nucleic acid molecules capable of detecting polymorphisms present in an *Arabidopsis* mapping population according to claim 18, wherein said collection non-identical nucleic acid molecules is capable of detecting at  
15 least 25 polymorphisms are insertion or deletion polymorphisms.

21. The collection of non-identical nucleic acid molecules capable of detecting polymorphisms present in an *Arabidopsis* mapping population according to claim 518, wherein said collection of non-identical nucleic acid molecules is capable of detecting at  
20 least 50 polymorphisms selected from the group consisting of Table A.

22. The collection of non-identical nucleic acid molecules capable of detecting polymorphisms present in an *Arabidopsis* mapping population according to claim 21, wherein said collection of non-identical nucleic acid molecules is capable of detecting at  
25 least 100 polymorphisms selected from the group consisting of Table A.

23. The collection of non-identical nucleic acid molecules capable of detecting polymorphisms present in an *Arabidopsis* mapping population according to claim 18, wherein said collection of non-identical nucleic acid molecules is deposited on a substrate.

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24. Computer readable medium having recorded thereon at least 100 of the polymorphisms set forth in Table A.

25. A method of introgressing a trait of interest into a plant comprising using a  
10 nucleic acid marker for marker assisted selection of said plant, said nucleic acid marker capable of detecting a polymorphism selected from Table A, and introgressing said trait into said plant.

26. A method for identifying transposons in the DNA of an organism comprising  
15 identifying INDELs in said DNA and comparing the sequence of said INDELs to the sequence of one or more known transposons.

Adapted